

RAW SEQUENCE LISTING

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Application Serial Number: 10/539,723
Source: PCT/0
Date Processed by STIC: 2/12/05

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PCT

RAW SEQUENCE LISTING DATE: 07/12/2005
PATENT APPLICATION: US/10/539,723 TIME: 10:02:55

Input Set : N:\RJAVED\10539723.txt
Output Set: N:\CRF4\07122005\J539723.raw

3 <110> APPLICANT: Bayer CropScience GmbH
 5 <120> TITLE OF INVENTION: Plant cells and plants which synthesize a starch with an
 increased final
 6 viscosity
 8 <130> FILE REFERENCE: BCS 02 5002 - PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/539,723
 C--> 10 <141> CURRENT FILING DATE: 2005-06-20
 10 <150> PRIOR APPLICATION NUMBER: EP 02028530.0
 11 <151> PRIOR FILING DATE: 2002-12-19
 13 <150> PRIOR APPLICATION NUMBER: EP 03090275.3
 14 <151> PRIOR FILING DATE: 2003-08-29
 16 <160> NUMBER OF SEQ ID NOS: 8
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 4167
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Solanum tuberosum
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (207)..(3899)
 28 <223> OTHER INFORMATION:
 31 <300> PUBLICATION INFORMATION:
 32 <301> AUTHORS: Abel,G.J., Springer,F., Willmitzer,L. and Kossmann,J.
 33 <302> TITLE: Cloning and functional analysis of a cDNA encoding a novel 139 kDa
 34 <303> JOURNAL: Plant J.
 35 <304> VOLUME: 10
 36 <305> ISSUE: 6
 37 <306> PAGES: 981-991
 38 <307> DATE: 1996
 39 <308> DATABASE ACCESSION NO: X94400
 40 <309> DATABASE ENTRY DATE: 1995-12-22
 41 <313> RELEVANT RESIDUES: (1)..(4167)
 43 <300> PUBLICATION INFORMATION:
 44 <308> DATABASE ACCESSION NO: EMBL / X94400
 45 <309> DATABASE ENTRY DATE: 1997-04-16
 46 <313> RELEVANT RESIDUES: (1)..(4167)
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 53 gatgttctat ttgattctgt ggtgaacaag agttttacaa agaacattcc tttttctttt 180
 55 tttcttggtt ctgtgtggg tcagcc atg gat gtt cca ttt cca ctg cat aga 233
 56 Met Asp Val Pro Phe Pro Leu His Arg
 57 1 5
 59 cca ttq aqt tqc aca aqt qtc tcc aat qca ata acc cac ctc aaq atc 281

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64	Lys	Pro	Phe	Leu	Gly	Phe	Val	Ser	His	Gly	Thr	Thr	Ser	Leu	Ser	Val	
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67	caa	tct	tct	tca	tgg	agg	aag	gat	gga	atg	gtt	act	ggg	gtt	tca	ttt	377
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71	cca	ttt	tgt	gca	aat	ctc	tcg	gga	aga	aga	cgg	aga	aaa	gtt	tca	act	425
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75	act	agg	agt	caa	gga	tct	tca	cct	aag	ggg	ttt	gtg	cca	agg	aag	ccc	473
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77							75				80				85		
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92	Val	Val	Arg	Asp	His	Lys	Phe	Leu	Glu	Asp	Glu	Asp	Glu	Ile	Asn	Gly	
93							140				145				150		
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107	ata	aga	caa	agt	gga	tct	cag	ggg	gaa	act	aat	gcc	agt	agc	aag	857	
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120	Lys	Gly	Pro	Val	Ala	Ser	Lys	Leu	Leu	Glu	Ile	Thr	Lys	Ala	Ser	Asp	
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123	gtg	gaa	cac	act	gaa	agc	aat	gag	att	gtt	gac	tta	gac	act	aat	agt	1049
124	Val	Glu	His	Thr	Glu	Ser	Asn	Glu	Ile	Asp	Asp	Leu	Asp	Thr	Asn	Ser	

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127 ttc ttt aaa tca gat tta att gaa gag gag gat gag cca tta gct gca gga				1097
128 Phe Phe Lys Ser Asp Leu Ile Glu Glu Asp Glu Pro Leu Ala Ala Gly				
129 285	290	295		
131 aca gtg gag act gga gat tct tct cta aac tta aga ttg gag atg gaa				1145
132 Thr Val Glu Thr Gly Asp Ser Ser Leu Asn Leu Arg Leu Glu Met Glu				
133 300	305	310		
135 gca aat cta cgt agg cag gct ata gaa agg ctt gcc gag gaa aat tta				1193
136 Ala Asn Leu Arg Arg Gln Ala Ile Glu Arg Leu Ala Glu Glu Asn Leu				
137 315	320	325		
139 ttg caa ggg atc aga tta ttt tgt ttt cca gag gtt gta aaa cct gat				1241
140 Leu Gln Gly Ile Arg Leu Phe Cys Phe Pro Glu Val Val Lys Pro Asp				
141 330	335	340	345	
143 gaa gat gtc gag ata ttt ctt aac aga ggt ctt tcc act ttg aag aat				1289
144 Glu Asp Val Glu Ile Phe Leu Asn Arg Gly Leu Ser Thr Leu Lys Asn				
145 350	355	360		
147 gag tct gat gtc ttg att atg gga gct ttt aat gag tgg cgc tat agg				1337
148 Glu Ser Asp Val Leu Ile Met Gly Ala Phe Asn Glu Trp Arg Tyr Arg				
149 365	370	375		
151 tct ttt act aca agg cta act gag act cat ctc aat gga gat tgg tgg				1385
152 Ser Phe Thr Thr Arg Leu Thr Glu Thr His Leu Asn Gly Asp Trp Trp				
153 380	385	390		
155 tct tgc aag atc cat gtt ccc aag gaa gca tac agg gct gat ttt gtg				1433
156 Ser Cys Lys Ile His Val Pro Lys Glu Ala Tyr Arg Ala Asp Phe Val				
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159 ttt ttt aat gga caa gat gtc tat gac aac aat gat gga aat gac ttc				1481
160 Phe Phe Asn Gly Gln Asp Val Tyr Asp Asn Asn Asp Gly Asn Asp Phe				
161 410	415	420	425	
163 agt ata act gtg aaa ggt ggt atg caa atc att gac ttt gaa aat ttc				1529
164 Ser Ile Thr Val Lys Gly Gly Met Gln Ile Ile Asp Phe Glu Asn Phe				
165 430	435	440		
167 ttg ctt gag gag aaa tgg aga gaa cag gag aaa ctt gct aaa gaa caa				1577
168 Leu Leu Glu Glu Lys Trp Arg Glu Gln Glu Lys Leu Ala Lys Glu Gln				
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172 Ala Glu Arg Glu Arg Leu Ala Glu Glu Gln Arg Arg Ile Glu Ala Glu				
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176 Lys Ala Glu Ile Glu Ala Asp Arg Ala Gln Ala Lys Glu Glu Ala Ala				
177 475	480	485		
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180 Lys Lys Lys Val Leu Arg Glu Leu Met Val Lys Ala Thr Lys Thr				
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183 cgt gat atc acg ttg tac ata gag cca agt gaa ttt aaa tgc gag gac				1769
184 Arg Asp Ile Thr Trp Tyr Ile Glu Pro Ser Glu Phe Lys Cys Glu Asp				
185 510	515	520		
187 aag gtc agg tta tac tat aac aaa agt tca ggt cct ctc tcc cat gct				1817
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189 525	530	535		

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191 aag gac ttg atc cac gga gga tat aat aat tgg aag gat ggt ttg	1865
192 Lys Asp Leu Trp Ile His Gly Gly Tyr Asn Asn Trp Lys Asp Gly Leu	
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195 tct att gtc aaa aag ctt gtt aaa tct gag aga ata gat ggt gat tgg	1913
196 Ser Ile Val Lys Lys Leu Val Lys Ser Glu Arg Ile Asp Gly Asp Trp	
197 555 560 565	
199 tgg tat aca gag gtt gtt att cct gat cag gca ctt ttc ttg gat tgg	1961
200 Trp Tyr Thr Glu Val Val Ile Pro Asp Gln Ala Leu Phe Leu Asp Trp	
201 570 575 580 585	
203 gtt ttt gct gat ggt cca ccc aag cat gcc att gct tat gat aac aat	2009
204 Val Phe Ala Asp Gly Pro Pro Lys His Ala Ile Ala Tyr Asp Asn Asn	
205 590 595 600	
207 cac cgc caa gac ttc cat gcc att gtc ccc aac cac att ccg gag gaa	2057
208 His Arg Gln Asp Phe His Ala Ile Val Pro Asn His Ile Pro Glu Glu	
209 605 610 615	
211 tta tat tgg gtt gag gaa gaa cat cag atc ttt aag aca ctt cag gag	2105
212 Leu Tyr Trp Val Glu Glu His Gln Ile Phe Lys Thr Leu Gln Glu	
213 620 625 630	
215 gag aga agg ctt aga gaa gcg gct atg cgt gct aag gtt gaa aaa aca	2153
216 Glu Arg Arg Leu Arg Glu Ala Ala Met Arg Ala Lys Val Glu Lys Thr	
217 635 640 645	
219 gca ctt ctg aaa act gaa aca aag gaa aga act atg aaa tca ttt tta	2201
220 Ala Leu Leu Lys Thr Glu Thr Lys Glu Arg Thr Met Lys Ser Phe Leu	
221 650 655 660 665	
223 ctg tct cag aag cat gta gta tat act gag cct ctt gat atc caa gct	2249
224 Leu Ser Gln Lys His Val Val Tyr Thr Glu Pro Leu Asp Ile Gln Ala	
225 670 675 680	
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228 Gly Ser Ser Val Thr Val Tyr Tyr Asn Pro Ala Asn Thr Val Leu Asn	
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232 Gly Lys Pro Glu Ile Trp Phe Arg Cys Ser Phe Asn Arg Trp Thr His	
233 700 705 710	
235 cgc ctg ggt cca ttg cca cct cag aaa atg tcg cct gct gaa aat ggc	2393
236 Arg Leu Gly Pro Leu Pro Pro Gln Lys Met Ser Pro Ala Glu Asn Gly	
237 715 720 725	
239 acc cat gtc aga gca act gtg aag gtt cca ttg gat gca tat atg atg	2441
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241 730 735 740 745	
243 gat ttt gta ttt tcc gag aga gaa gat ggt ggg att ttt gac aat aag	2489
244 Asp Phe Val Phe Ser Glu Arg Glu Asp Gly Gly Ile Phe Asp Asn Lys	
245 750 755 760	
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248 Ser Gly Met Asp Tyr His Ile Pro Val Phe Gly Gly Val Ala Lys Glu	
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251 cct cca atg cat att gtc cat att gct gtc gaa atg gca cca att gca	2585
252 Pro Pro Met His Ile Val His Ile Ala Val Glu Met Ala Pro Ile Ala	
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28